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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=6; day=9; hr=15; min=26; sec=45; ms=624;]

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Application No: 10567073

Version No: 3.0

Input Set:

Output Set:

Started: 2010-06-03 10:06:30.535

Finished: 2010-06-03 10:06:31.548

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 13 ms

Total Warnings: 11

Total Errors: 0

No. of SeqIDs Defined: 14

Actual SeqID Count: 14

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (13)
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SEQUENCE LISTING

<110> UMBI
Bryan, Philip N.

<120> Engineered Proteases for Affinity Purification and Processing of
Fusion Proteins

<130> 4115-181

<140> 10567073

<141> 2006-03-07

<150> US 60/493,032

<151> 2003-08-06

<150> PCT/US04/021049

<151> 2004-06-29

<160> 14

<170> PatentIn version 3.5

<210> 1

<211> 30

<212> PRT

<213> Bacillus amyloliquefaciens

<400> 1

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Ile	Phe	Thr	Met	Ala	Phe	Gly	Ser	Thr	Ser	Ser	Ala	Gln	Ala
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<212> PRT

<213> Bacillus amyloliquefaciens

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Ala	Gly	Lys	Ser	Asn	Gly	Glu	Lys	Lys	Tyr	Ile	Val	Gly	Phe	Lys	Gln
1				5					10					15	

Thr	Met	Ser	Thr	Met	Ser	Ala	Ala	Lys	Lys	Lys	Asp	Val	Ile	Ser	Glu
			20						25					30	

Lys	Gly	Gly	Lys	Val	Gln	Lys	Gln	Phe	Lys	Tyr	Val	Asp	Ala	Ala	Ser
			35					40							45

Ala Thr Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser
50 55 60

Val Ala Tyr Val Glu Glu Asp His Val Ala His Ala Tyr
65 70 75

<210> 3

<211> 275

<212> PRT

<213> Bacillus amyloliquefaciens

<400> 3

Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu
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His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp
20 25 30

Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala
35 40 45

Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His
50 55 60

Gly Thr His Val Ala Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly
65 70 75 80

Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu
85 90 95

Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
100 105 110

Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
115 120 125

Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala
130 135 140

Ser Gly Val Val Val Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly
145 150 155 160

Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala

165

170

175

Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val
 180 185 190

Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
 195 200 205

Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser
 210 215 220

Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn
 225 230 235 240

Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu Asn Thr Thr Thr Lys
 245 250 255

Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala
 260 265 270

Ala Ala Gln
 275

<210> 4

<211> 75

<212> PRT

<213> Artificial Sequence

<220>

<223> pR8 variant of SEQ ID NO: 2

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Ala Gly Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Ser
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Gly Ile Lys Ser Cys Ala Lys Lys Gln Asp Val Ile Ser Glu Lys Gly
 20 25 30

Gly Lys Leu Gln Lys Cys Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr
 35 40 45

Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala
 50 55 60

Tyr Val Glu Glu Asp Lys Val Ala Lys Ala Tyr
65 70 75

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<212> PRT
<213> Artificial Sequence

<220>
<223> pR8FKAM variant of SEQ ID NO: 2

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Ala Gly Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Ser
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Gly Ile Lys Ser Cys Ala Lys Lys Gln Asp Val Ile Ser Glu Lys Gly
20 25 30

Gly Lys Leu Gln Lys Cys Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr
35 40 45

Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala
50 55 60

Tyr Val Glu Glu Asp Lys Val Phe Lys Ala Met
65 70 75

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<212> PRT
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Gly Ile Lys Ser Cys Ala Lys Lys Gln Asp Val Ile Ser Glu Lys Gly
20 25 30

Gly Lys Leu Gln Lys Cys Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr
35 40 45

Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala

Tyr Val Glu Glu Asp Lys Val Phe Arg Ala Met
65 70 75

<210> 7
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<220>
<223> C-terminal portion of prodomain

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<221> VARIANT
<222> (6)..(6)
<223> Xaa is Phe or Tyr

<220>
<221> VARIANT
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<223> Xaa is Met, Lys or Tyr

<400> 7

Glu Glu Asp Lys Leu Xaa Gln Ser Xaa
1 5

<210> 8
<211> 6
<212> PRT
<213> Artificial Sequence

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<223> Residues 16-21 of SEQ ID NO: 2

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Gln Thr Met Ser Thr Met
1 5

<210> 9
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Substitution of residues 16-21 of subtilisin prodomain

<400> 9

Ser Gly Ile Lys

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<210> 10

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Substitution of P1-P4 of subtilisin prodomain

<400> 10

Phe Lys Ala Met

1

<210> 11

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Substitution of P1-P4 of subtilisin prodomain

<400> 11

Phe Lys Ala Tyr

1

<210> 12

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Substitution of P1-P4 of subtilisin prodomain

<400> 12

Phe Lys Ala Phe

1

<210> 13

<211> 4

<212> PRT

<213> Artificial Sequence

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<223> P1-P4 of wild-type subtilisin prodomain

<400> 13

Ala His Ala Tyr

1

<210> 14

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Substitution of P1-P4 of subtilisin prodomain

<400> 14

Phe Arg Ala Met

1